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DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 18.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strubeberg R.;
RT Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC018048; AAI18048.1;
DR PRINTS: PRO1641; PROMCHFAMILY.
KM Hypothetical protein.
SO SEQUENCE 165 AA; 18679 MW; 2339E8938BEC499 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRCLMGRVYRRCMV 16
DB 150 LRCLMGRVYRRCMV 165
|||||
OY 09D220 PRELIMINARY; PRT; 165 AA.
ID 09D220
AC 09D220;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE A230109K23RLK protein.
DE A230109K23RLK protein.
GN A230109K23RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HYPOPHALAMUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bonfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guerninich S., Hill D., Hornann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaver-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL: AK020723; BAB32189.1;
DR MGD: MGI:1925014; A230109K23RLK.
DR PRINTS: PRO1641; PROMCHFAMILY.
SO SEQUENCE 165 AA; 18516 MW; 1872B6B1D4BEAC2 CRC64;

Query Match 100.0%; Score 95; DB 11; Length 165;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LRCLMGRVYRRCMV 16
DB 150 LRCLMGRVYRRCMV 165
|||||
OY 091916 PRELIMINARY; PRT; 150 AA.
ID 091916
AC 091916;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Melanin-concentrating hormone-like protein.
DE Paralicthys olivaceus (Flounder).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorphi; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Jeon J., Lee J., Song Y.;
RT "Melanin-concentrating hormone-like protein."
RT Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF236090; AAF67166.1;
DR PRINTS: PRO1641; PROMCHFAMILY.
SO SEQUENCE 150 AA; 16913 MW; 117A280F46ED4499 CRC64;

Query Match 90.5%; Score 86; DB 13; Length 150;
Best Local Similarity 86.7%; Pred. No. 4,5e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRCLMGRVYRRCMV 15
DB 131 LRCLMGRVYRRCMV 145
|||||
OY 09B0D1 PRELIMINARY; PRT; 86 AA.
ID 09B0D1
AC 09B0D1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Pro-melanin-concentrating hormone-like 2 protein.
GN PCHL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE=21108351; PubMed=1181993;
RA Counseaux A., Nelson J.L.;
RT "Birth of two chimeric genes in the Homiidae lineage."
RT Science 291:1293-1297(2001).
DR EMBL: AY008413; AAK31297.1;
DR EMBL: AY028320; AAK31290.1;
DR EMBL: AY008412; AAK31296.1;
DR PRINTS: PRO1641; PROMCHFAMILY.
SO SEQUENCE 86 AA; 9856 MW; 1C8D69B786B47471 CRC64;

Query Match 81.1%; Score 77; DB 4; Length 86;
Best Local Similarity 86.7%; Pred. No. 9,1e-06;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LRCLMGRVYRRCMV 16
DB 72 LRCLMGRVYRRCMV 86
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Db 33 KCEVCGKVFETCWMOL 47

RESULT 8
ID 08X2X6 PRELIMINARY; PRT: 186 AA.
AC 08X2X6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein ECS4988.
GN ECS4988.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxId=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
R Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobé T.,
RA Ikeda T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,
R Kihara S., Shibata T., Hatgori M., Shinagawa H.;
RT Complete genome sequence of enterohemorrhagic Escherichia coli
OT O157:H7 and genomic comparison with a laboratory strain K-12.*;
RL DNA Res. 8:11-22(2001)
DR ENBL:AP02567; BAB38411.1; -
SQ SEQUENCE 186 AA; 21454 MW; CSEDEL66BCA9989 CRC64;

Query Match 46.8%; Score 44.5; DB 16; Length 186;
Best Local Similarity 57.1%; Pred. NO. 6.6;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1

Dd 159 LECTINr-YKPMQ 171
ID 1 ILCMGRYRPPQC 15
AC 09DJR4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 4933439J1IRIK protein.
GN 4933439J1IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shimagawa A., Shishida Y., Konno H., Adachi J., Fukuda S.,
RA Akakura T., Hara A., Fukuishi Y., Kono H., Adachi J., Yamanka I.,
RA Aizawa K., Izawa M., Nishik K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Salto R.,
R Kadota K., Matsuda H.A., Ashburner M., Batclav S., Casavant T.,
R Fleischmann W., Gaasterland T., Glisz C., King B., Koehiva H.,
R Knehl P., Lewis S., Matsuo T., Nikaido I., Resole G., Quackenbush J.,
R Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barns G.,
R Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
R Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
R Gustincich S., Hall D., Hofman M., Humé D.A., Kamiya M., Lee N.H.,
R Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombearts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,

RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK017132; BAB30509.1; -
 DR MGI:1918557; 493343901RLK.
 SQ SEQUENCE 154 AA; 17921 MW; 9189DCAC8434C49 CRC64;

Query Match 46.3%; Score 44; DB 11; Length 154;
 Best Local Similarity 61.5%; Pred. No. 6.7;
 Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 OY 4 CML-GRVYRCW 14
 DB 127 CMLGRVYRCW 139

RESULT 10
 ID 076862 PRELIMINARY; PRT: 397 AA.
 AC 076862;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE EG:100610.2 protein.
 GN EG:100610.2 OR CG2681.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;
 RT Sequencing the distal x chromosome of Drosophila melanogaster.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RA Benos P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL023874; CA119647.1; -
 DR Flybase: FBgn0024997; EG:100610.2.
 DR InterPro: IPR004162; Sina.
 DR Pfam: PF03145; Sina; 1.
 SQ SEQUENCE 397 AA; 44818 MW; 98AA3314F8494565 CRC64;

Query Match 45.8%; Score 43.5; DB 5; Length 397;
 Best Local Similarity 46.7%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

OY 2 LRCMLGRVYRCW-NO 15
 DB 62 MKCFGRVYRCW-NO 76

RESULT 11
 ID 09W4M4 PRELIMINARY; PRT: 414 AA.
 AC 09W4M4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE EG:100610.2 protein.
 GN EG:100610.2 OR CG2681.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE:20196006; Pubmed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.A.,
 RA Branton R.C., Rogers J.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borovda D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibovyan C.,
 RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kenton S., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei T., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltai B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle B.J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relbert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Sliker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Ventier E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003425; AAF45811.1; -
 DR Flybase: FBgn0024997; EG:100610.2.
 DR InterPro: IPR004162; Sina.
 DR Pfam: PF03145; Sina; 1.
 SQ SEQUENCE 414 AA; 46719 MW; 0E70A32A08B77640 CRC64;

Query Match 45.8%; Score 43.5; DB 5; Length 414;
 Best Local Similarity 46.7%; Pred. No. 21;
 Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

OY 2 LRCMLGRVYRCW-NO 15
 DB 79 MKCFGRVYRCW-NO 93

RESULT 12
 ID 0951L0 PRELIMINARY; PRT: 103 AA.
 AC 0951L0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE Hypothetical 11.3 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID:9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA Hashimoto K., Oada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
 RA Terao K., Sugano S.;
 RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
 libraries.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AB072778; BAB69747.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 103 AA; 11326 MW; D8547BDDA4141195 CRC64;

Query Match 44.2%; Score 42; DB 6; Length 103;
 Best Local Similarity 46.2%; Pred. No. 10;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 CMLGRVYRPMQOV 16
 Db 52 CGLGLSNPCWRL 64

RESULT 13

P71972 PRELIMINARY; PRT; 250 AA.

AC P71972;
 DT 01-JUN-1998 (TREMBLrel. 05, Created)
 DT 01-MAR-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein RV2675C.
 GN RV2675C OR MTCY441.44C OR MT3749.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekle F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentsle S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers K.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares K.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.
 RL Nature 393:537-544(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG IN C-TERMINAL REGION TO M.LEPRAE U17642.
 DR EMBL: Z80225; CAB0228.1; -.
 DR EMBL: AF007105; AAK47064.1; -.
 DR TIGR: MT2749; -.
 DR TubercuList: RV2675C; -.
 DR InterPro: IPR000051; SAM_bind.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 27545 MW; 2EC9718C7550F32C CRC64;

Query Match 44.2%; Score 42; DB 16; Length 250;
 Best Local Similarity 33.3%; Pred. No. 23;
 Matches 9; Conservative 4; Mismatches 2; Indels 12; Gaps 1;

OY 2 LRCML-----GRVYRPMQOV 16
 Db 218 VRCVLEFRRAIKPMLVGRVHAPFMEV 244

RESULT 14

ID O9GS12 PRELIMINARY; PRT; 311 AA.

AC O9GS12;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE F56H6.13 protein.
 GN F56H6.13.
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Kershaw J.K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: Z81553; CAC14333.1; -.
 SQ SEQUENCE 311 AA; 36614 MW; 4A9360CE41C1027B CRC64;

Query Match 44.2%; Score 42; DB 5; Length 311;
 Best Local Similarity 33.3%; Pred. No. 29;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRPMQOV 16
 Db 155 MRCVETRYNGIWMN 169

RESULT 15

O91HR4 PRELIMINARY; PRT; 555 AA.

AC O91HR4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Glycoprotein E (Fragment).
 OS Pseudorabies virus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10345;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-GUANGDONG;
 RA Lou G.M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF403050; AAK95640.1; -.
 DR InterPro: IPR003404; Herpes_glycopE.

DR Pfam: PF02480; Herpes_gE; 1.
 FT NON_TER 1
 FT NON_TER 555
 SQ SEQUENCE 555 AA; 59871 MW; 79CBEF2F03003CDB CRC64;

Query Match 44.2%; Score 42; DB 12; Length 555;
 Best Local Similarity 63.6%; Pred. No. 50;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 RCMGLGRVYRPMQOV 13
 Db 252 RCLLYIVYRPMQOV 262

Search completed: June 25, 2003, 11:54:02
 Job time : 40.04 secs